

SEQUENCE LISTING

<110> Ebner, Reinhard
Ruben, Steven

<120> Interleukins-21 and 22

<130> PF470P1

<150> 60/169,837

<151> 1999-12-09

<150> 09/320,713

<151> 1999-05-27

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<151> 1998-05-29

<150> 60/099,805

<151> 1998-09-10

<150> 60/131,965

<151> 1999-04-30

<150> PCT US99/11644

<151> 1999-05-27

<160> 32

<170> PatentIn version 3.0

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<212> DNA

<213> HOMO SAPIENS

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gcc gag tgc ctg tgc aga ggc tgt atc gat gca cgg acg ggc cgc gag	97
Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu	
20 25 30	

aca gct gcg ctc aac tcc gtg cgg ctg ctc cag agc ctg ctg gtg ctg	145
Thr Ala Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu	
35 40 45	

cgc cgc cgg ccc tgc tcc cgc gac ggc tcg ggg ctc ccc aca cct ggg	193
Arg Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly	
50 55 60	

gcc ttt gcc ttc cac acc gag ttc atc cac gtc ccc gtc ggc tgc acc	241
Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr	
65 70 75 80	

tgc gtg ctg ccc cgt tca gtg tgaccgccaa ggccgtgggg cccttagact	292
Cys Val Leu Pro Arg Ser Val	
85	

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ggacacgtgt gctccccaga gggcaccccc tatttatgtg tatttattgt tatttatatg 352
cctcccccaa cactaccctt ggggtctggg cattccccgt gtctggagga cagcccccca 412
ctgttctcct catctccagc ctacgtagtt gggggtwgaa ggagctcagc acctcttcca 472
gcccttaaag ctgcagaaaa ggtgtcacac ggctgcctgt acctgggyc cctgtcctgc 532
tcccggcttc ccttacccta tcaactggcct caggcccccg caggctgcct cttcccaacc 592
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Ala Arg Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe
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Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu
20          25          30

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Thr Ala Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu
35          40          45

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Arg Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly
50          55          60

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Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr
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Cys Val Leu Pro Arg Ser Val
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  1          5          10          15

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ctg cag ctg ggg ccg cgt gag cag gcg cgc aac gcg agc tgc ccg gca 95
Leu Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala
20          25          30

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ggg ggc agg ccc gcc gac cgc cgc ttc cgg ccg ccc acc aac ctg cgc Gly Gly Arg Pro Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg 35 40 45	143
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ccc agg tac ctg cct gaa gcc tac tgc ctg tgc cgg ggc tgc ctg acc Pro Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr 65 70 75	239
ggg ctg ttc ggc gag gag gac gtg cgc ttc cgc agc gcc cct gtc tac Gly Leu Phe Gly Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr 80 85 90 95	287
atg ccc acc gtc gtc ctg cgc cgc acc ccc gcc tgc gcc ggc ggc cgt Met Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg 100 105 110	335
tcc gtc tac acc gag gcc tac gtc acc atc ccc gtg ggc tgc acc tgc Ser Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys 115 120 125	383
gtc ccc gag ccg gag aag gac gca gac agc atc aac tcc agc atc gac Val Pro Glu Pro Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp 130 135 140	431
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accaagtgcc ggagcaccag cgccgccttt ccatggagac tcgtaagcag cttcatctga	652
cacgggcatc cctggcttgc ttttagctac aagcaagcag cgtggctgga agctgatggg	712
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Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly
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Gly Arg Pro Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser
35 40 45

Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro
50 55 60

Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly
65 70 75 80

Leu Phe Gly Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met
85 90 95

Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser
100 105 110

Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val
115 120 125

Pro Glu Pro Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys
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Gln Gly Ala Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
145 150 155 160

<210> 5
<211> 155
<212> PRT
<213> HOMO SAPIENS

<400> 5

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Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly
20 25 30
Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
35 40 45
Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
50 55 60
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
65 70 75 80
Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
85 90 95
Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
100 105 110
Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
115 120 125
Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
130 135 140
Thr Cys Val Thr Pro Ile Val His His Val Ala
145 150 155

<210> 6

<211> 158

<212> PRT

<213> MUS MUSCULUS

<400> 6

Met Ser Pro Gly Arg Ala Ser Ser Val Ser Leu Met Leu Leu Leu Leu
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20 25 30
Ser Ala Cys Pro Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys
35 40 45
Val Asn Leu Lys Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg
50 55 60
Arg Pro Ser Asp Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His
65 70 75 80
Arg Asn Glu Asp Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln
85 90 95
Cys Arg His Gln Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His
100 105 110
Met Asn Ser Val Leu Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu
115 120 125
Pro Glu Ser Cys Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly

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Val Gly Cys Thr Cys Val Ala Ser Ile Val Arg Gln Ala Ala
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<213> VIRAL

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Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu Leu Leu Ser Ile
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Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln Thr Pro Arg Cys
20              25              30

Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met Val Thr Leu Ser
35              40              45

Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser Asp Tyr Tyr Asn
50              55              60

Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg
65              70              75              80

Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val
85              90              95

Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln
100             105             110

Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser
115             120             125

Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys Thr Cys Val Thr
130             135             140

Pro Ile Val His Asn Val Asp
145             150

<210> 8
<211> 180
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<213> HOMO SAPIENS

<400> 8

Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile Phe
1              5              10              15

Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln
20              25              30

Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp
35              40              45

Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg
50              55              60

Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala
65              70              75              80
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Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg
85 90 95

Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile
100 105 110

Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn
115 120 125

Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe
130 135 140

Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr
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Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys
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Thr Cys Ile Phe
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<210> 9
<211> 45
<212> DNA
<213> OLIGONUCLEOTIDE

<220>
<221> primer_bind
<222> (1)..(45)
<223> 5' primer containing a BamHI restriction site followed by
several nucleotides of the amino terminal coding
sequence of mature IL-21 sequence

<400> 9
gatcgcggtat cgcacacgga tgaggaccgc tatccacaga agctg

45

<210> 10
<211> 41
<212> DNA
<213> OLIGONUCLEOTIDE

<220>
<221> primer_bind
<222> (1)..(41)
<223> 3' primer containing an HindIII restriction site followed by
several nucleotides complementary to the 3' end of the
coding sequence of IL-21 DNA sequence.

<400> 10
cccaagcttt cacactgaac ggggcagcac gcaggtgcag c

41

<210> 11
<211> 35
<212> DNA
<213> OLIGONUCLEOTIDE

<220>
<221> primer_bind
<222> (1)..(35)
<223> 5' primer containing a BamHI restriction site, a "C" residue

to preserve the reading frame, and 16 nucleotides of the sequence of the complete IL-21 protein.

<400> 11
cgccgcggat cgcctatccg cagcagtgga cagcg 35

<210> 12
<211> 29
<212> DNA
<213> OLIGONUCLEOTIDE

<220>
<221> primer_bind
<222> (1)..(29)
<223> 3' primer containing an Asp718 restriction site, and 20 nucleotides complementary to the 3' noncoding sequence of IL-21.

<400> 12
cgcggtaccc actgaacggg gcagcacgc 29

<210> 13
<211> 733
<212> DNA
<213> HOMO SAPIENS

<400> 13
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tctcccgga tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcgaagg tctccaacaa agccctccca acccccatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga 540
ccacgcctcc cgtgctggac tccgacgggt ccttcttctt ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggetctgc 660
acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat 733

<210> 14
<211> 5
<212> PRT
<213> HOMO SAPIENS

<220>

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<221> SITE
 <222> (1)..(5)
 <223> Xaa is equal to any amino acid

<400> 14

Trp Ser Xaa Trp Ser
 1 5

<210> 15
 <211> 86
 <212> DNA
 <213> OLIGONUCLEOTIDE

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 <221> primer_bind
 <222> (1)..(86)
 <223> 5' primer containing 14 tandem copies of the GAS-binding site, 18bp of complementary sequence to SV40 early promotor sequence, and is flanked with an XhoI restriction site.

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 cccgaaatat ctgccatctc aattag 86

<210> 16
 <211> 27
 <212> DNA
 <213> OLIGONUCLEOTIDE

<220>
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 <222> (1)..(27)
 <223> 3' primer containing a complementary sequence to SV40 promotor and flanked with an Hin dIII site.

<400> 16
 gcggcaagct ttttgcaaag cctaggc 27

<210> 17
 <211> 271
 <212> DNA
 <213> HOMO SAPIENS

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 gccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
 ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
 ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 18

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<211> 32
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 <223> 5' PCR primer.

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32

<210> 19
 <211> 31
 <212> DNA
 <213> OLIGONUCLEOTIDE

<220>
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 <222> (1)..(31)
 <223> 3' PCR primer.

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 gcgaagcttc gcgactcccc ggatccgcct c

31

<210> 20
 <211> 12
 <212> DNA
 <213> OLIGONUCLEOTIDE

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 <222> (1)..(12)
 <223> NF-kappaB binding site.

<400> 20
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12

<210> 21
 <211> 73
 <212> DNA
 <213> OLIGONUCLEOTIDE

<220>
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 <222> (1)..(73)
 <223> 5' primer containing 4 tandem copies of the NF-kappaB binding site, 18bp of complementary sequence to 5' end of SV40 promotor sequence, flanked by an XhoI restriction site.

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60

ccatctcaat tag

73

<210> 22

<211> 27
 <212> DNA
 <213> OLIGONUCLEOTIDE

<220>
 <221> primer_bind
 <222> (1)..(27)
 <223> 3' primer containing sequence complementary to the 3' end of the SV40 promotor and flanked by an HindIII restriction site.

<400> 22
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<210> 23
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 <212> DNA
 <213> HOMO SAPIENS

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 cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180
 ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240
 cttttgcaaa aagctt 256

<210> 24
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 <222> (11)..(11)
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 cntaattggg a 371

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<220>
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<220>
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 <222> (251)..(251)
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<220>
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 ctgccccggg aggtctcccc ggnccccgcat cccgaggcgc ccaagctgga gccgcctgga 180
 ggnttcggtc ggcgactctg aagagagtnc accgagcaaa ccaagtgccg gagcaacagc 240
 gncgnctttt ncatggagat tcgtaagcan ttttcatttg acanggggat ccctgggttg 300
 tttttagtta caagcaagca nntggnttga agtnngntggg gaaaggancc gnagggattc 360
 tgtnttnggg gccntntgga gggttttgga aaatttnagg gggtttctgn gggtttttta 420
 anattggntt tttttagggt tnaagggttn nttaacttgg gngtttttcn aanngttggg 480
 ggattntttt tnaagatt 498

<210> 26
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 <212> DNA
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<223> n is equal to any a, t, g, or c

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<223> n is equal to any a, t, g, or c

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<223> n is equal to any a, t, g, or c

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gttcagagac agactttcaa tctaaagaaa agatcaaggn cctagctctn gtggcagaat 120
gcagaaacag aagccnccag atnganctcn gcagatgcta acngggccca ctttgtcc 178

<210> 27
<211> 264
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<220>
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<223> n is equal to any a, t, g, or c

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<222> (131)..(131)
<223> n is equal to any a, t, g, or c

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<223> n is equal to any a, t, g, or c

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<223> n is equal to any a, t, g, or c

<400> 27
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cctgccccgg aaggtctccc cggcccgcat cccgaggcgc ccaagctgga gccgcctgga 120

gggcttcggt ncggcgaacc tctgaaagag aagtgccacc gagcaaacca agtgccggta 180
gcaccagngc cgcctttcca tggagactcg taagcagctt catctganac gggaatccct 240
ggtttgcttt tagctacaag caag 264

<210> 28
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<212> DNA
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<220>
<221> CDS
<222> (34) .. (624)

<400> 28
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Met Thr Leu Leu Pro Gly Leu
1 5

ctg ttt ctg acc tgg ctg cac aca tgc ctg gcc cac cat gac ccc tcc 102
Leu Phe Leu Thr Trp Leu His Thr Cys Leu Ala His His Asp Pro Ser
10 15 20

ctc agg ggg cac ccc cac agt cac ggt acc cca cac tgc tac tcg gct 150
Leu Arg Gly His Pro His Ser His Gly Thr Pro His Cys Tyr Ser Ala
25 30 35

gag gaa ctg ccc ctc ggc cag gcc ccc cca cac ctg ctg gct cga ggt 198
Glu Glu Leu Pro Leu Gly Gln Ala Pro Pro His Leu Leu Ala Arg Gly
40 45 50 55

gcc aag tgg ggg cag gct ttg cct gta gcc ctg gtg tcc agc ctg gag 246
Ala Lys Trp Gly Gln Ala Leu Pro Val Ala Leu Val Ser Ser Leu Glu
60 65 70

gca gca agc cac agg ggg agg cac gag agg ccc tca gct acg acc cag 294
Ala Ala Ser His Arg Gly Arg His Glu Arg Pro Ser Ala Thr Thr Gln
75 80 85

tgc ccg gtg ctg cgg ccg gag gag gtg ttg gag gca gac acc cac cag 342
Cys Pro Val Leu Arg Pro Glu Glu Val Leu Glu Ala Asp Thr His Gln
90 95 100

cgc tcc atc tca ccc tgg aga tac cgg gtg gac acg gat gag gac cgc 390
Arg Ser Ile Ser Pro Trp Arg Tyr Arg Val Asp Thr Asp Glu Asp Arg
105 110 115

tat cca cag aag ctg gcc ttc gcc gag tgc ctg tgc aga ggc tgt atc 438
Tyr Pro Gln Lys Leu Ala Phe Ala Glu Cys Leu Cys Arg Gly Cys Ile
120 125 130 135

gat gca cgg acg ggc cgc gag aca gct gcg ctc aac tcc gtg cgg ctg 486
Asp Ala Arg Thr Gly Arg Glu Thr Ala Ala Leu Asn Ser Val Arg Leu
140 145 150

ctc cag agc ctg ctg gtg ctg cgc cgc cgg ccc tgc tcc cgc gac ggc 534
Leu Gln Ser Leu Leu Val Leu Arg Arg Arg Pro Cys Ser Arg Asp Gly
155 160 165

tcg ggg ctc ccc aca cct ggg gcc ttt gcc ttc cac acc gag ttc atc 582
Ser Gly Leu Pro Thr Pro Gly Ala Phe Ala Phe His Thr Glu Phe Ile

Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu Arg Arg
145 150 155 160

Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe
165 170 175

Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val
180 185 190

Leu Pro Arg Ser Val
195

<210> 30
<211> 332
<212> DNA
<213> HOMO SAPIENS

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<223> n is equal to any a, t, g, or c

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<223> n is equal to any a, t, g, or c

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<223> n is equal to any a, t, g, or c

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<223> n is equal to any a, t, g, or c

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<223> n is equal to any a, t, g, or c

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 <222> (314)..(314)
 <223> n is equal to any a, t, g, or c

<400> 30
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 gctgtatcga tgcacggacg ggccgcgaga cagctgcgct caactccgtg cggctgctcc 120
 agagcctgac tgggtgctgcg ccgccggccc tgactaccgc cnacggacta cgggggctac 180
 cccacacctg gggncctttg accttccaca ccgnagttac atgccacgta ccccgttcgg 240
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 ccctnagtac tggnacacgt gtgatacccc ag 332

<210> 31
 <211> 522
 <212> DNA
 <213> HOMO SAPIENS

<220>
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 <222> (1)..(522)

<400> 31
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 Gly Cys Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg
 1 5 10 15
 ctg gcg gcc ggc gtg ctc agt gcc ttc cac cac acg ctg cag ctg ggg 96
 Leu Ala Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly
 20 25 30
 ccg cgt gag cag gcg cgc aac gcg agc tgc ccg gca ggg ggc agg ccc 144
 Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro
 35 40 45
 gcc gac cgc cgc ttc cgg ccg ccc acc aac ctg cgc agc gtg tgc ccc 192
 Ala Asp Arg Arg Phe Arg Pro Thr Asn Leu Arg Ser Val Ser Pro
 50 55 60
 tgg gcc tac aga atc tcc tac gac ccg gcg agg tac ccc agg tac ctg 240
 Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu
 65 70 75 80
 cct gaa gcc tac tgc ctg tgc cgg ggc tgc ctg acc ggg ctg ttc ggc 288
 Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly
 85 90 95
 gag gag gac gtg cgc ttc cgc agc gcc cct gtc tac atg ccc acc gtc 336
 Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val
 100 105 110
 gtc ctg cgc cgc acc ccc gcc tgc gcc ggc ggc cgt tcc gtc tac acc 384
 Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr
 115 120 125
 gag gcc tac gtc acc atc ccc gtg ggc tgc acc tgc gtc ccc gag ccg 432

Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro
130 135 140

gag aag gac gca gac agc atc aac tcc agc atc gac aaa cag ggc gcc 480
Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala
145 150 155 160

aag ctc ctg ctg ggc ccc aac gac gcg ccc gct ggc ccc tga 522
Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
165 170

<210> 32
<211> 173
<212> PRT
<213> HOMO SAPIENS

<400> 32

Gly Cys Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln Leu Tyr Gly Arg
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Leu Ala Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly
20 25 30

Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro
35 40 45

Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro
50 55 60

Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu
65 70 75 80

Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly
85 90 95

Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met Pro Thr Val
100 105 110

Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr
115 120 125

Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val Pro Glu Pro
130 135 140

Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys Gln Gly Ala
145 150 155 160

Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
165 170

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170	175	180	
cac gtc ccc gtc ggc tgc acc tgc gtg ctg ccc cgt tca gtg			624
His Val Pro Val Gly Cys Thr Cys Val Leu Pro Arg Ser Val			
185	190	195	
tgaccgccaa ggccgtgggg cccttagact ggacacgtgt gctccccaga gggcaccccc			684
tatttatgtg tatttattgt tatttatatg cctcccccaa cactaccctt ggggtctggg			744
cattccccgt gtctggagga cagcccccca ctgttctcct catctccagc ctcaagtagtt			804
gggggtwgaa ggagctcagc acctcttcca gcccttaaag ctgcagaaaa ggtgtcacac			864
ggctgcctgt accttgggyc cctgtcctgc tcccggcttc ccttacccta tcaactggcct			924
caggcccccg caggetgcct ctccccaacc tccttggaag taccctgttt tcttaaacaa			984
ttatttaagt gtacgtgtat tattaaactg atgaacacaa aaaaaaaaaa aaaaaaaaaa			1044
aaaaaaaaaa aaaaaaaaaa aaa			1067
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Leu Ala His His Asp Pro Ser Leu Arg Gly His Pro His Ser His Gly			
	20	25	30
Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly Gln Ala Pro			
	35	40	45
Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln Ala Leu Pro Val			
	50	55	60
Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His Arg Gly Arg His Glu			
65	70	75	80
Arg Pro Ser Ala Thr Thr Gln Cys Pro Val Leu Arg Pro Glu Glu Val			
	85	90	95
Leu Glu Ala Asp Thr His Gln Arg Ser Ile Ser Pro Trp Arg Tyr Arg			
	100	105	110
Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe Ala Glu			
	115	120	125
Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala			
	130	135	140